

# SEQUENCE LISTING

<110> Union Chimique Belge, S.A.  
Nocka, Karl  
Pirozzi, Gregory  
Einstein, Richard

<120> NOVEL GENES ASSOCIATED WITH ALLERGIC HYPERSENSITIVITY AND MAST CELL ACTIVATION

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<170> PatentIn version 3.1

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Pro Ala Leu Leu Glu Ala Ala Arg Ala Arg Tyr Glu Ser Leu His Ile  
15 20 25

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gac gac gag cgc gag ccc ccg gga ccc cca ggg gcc gcc ccg cca ccg Asp Asp Glu Arg Glu Pro Pro Gly Pro Pro Gly Ala Ala Pro Pro Pro 65 70 75	604
ccc cgc gcc ccg gac gca cag gag ccg gag gag gac gag gcc ggc gcg Pro Arg Ala Pro Asp Ala Gln Glu Pro Glu Glu Asp Glu Ala Gly Ala 80 85 90	652
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acc ggc ggt ccc acc cga aag atg ccc ccc agc gcc agt gcc gtg gac Thr Gly Gly Pro Thr Arg Lys Met Pro Pro Ser Ala Val Asp 110 115 120	748
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gtc cac ctg aag gaa ggt ggg ggc cca gat ggc ctg gat gcg ctg aag Val His Leu Lys Glu Gly Gly Gly Pro Asp Gly Leu Asp Ala Leu Lys 305 310 315	1324
aat aag ccc cag ctc cac agc atg gtg gcc agg agc ctg tgc cgg aac Asn Lys Pro Gln Leu His Ser Met Val Ala Arg Ser Leu Cys Arg Asn 320 325 330	1372
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gcc gct cac ctg agc tac atc tgc aga tac gat gac aaa tac agc aag Ala Ala His Leu Ser Tyr Ile Cys Arg Tyr Asp Asp Lys Tyr Ser Lys 445 450 455 460	1756
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aga ctc gtc aga gag ctg ctg gcc ttg gag gat gcc tct ccg acc cac	1948

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<211> 524  
<212> PRT  
<213> Homo sapiens

<400> 7

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Phe Gly Glu Ser Gly Pro Asp Ser Gly Gly Asn Pro Phe Tyr Ser Thr  
35 40 45

Ser Ala Ala Ser Arg Ser Ser Ser Ala Ala Ser Ser Asp Asp Glu Arg  
50 55 60

Glu Pro Pro Gly Pro Pro Gly Ala Ala Pro Pro Pro Arg Ala Pro  
65 70 75 80

Asp Ala Gln Glu Pro Glu Glu Asp Glu Ala Gly Ala Gly Trp Ser Ala  
85 90 95

Ala Leu Arg Asp Arg Pro Pro Pro Arg Phe Glu Asp Thr Gly Gly Pro  
100 105 110

Thr Arg Lys Met Pro Pro Ser Ala Ser Ala Val Asp Phe Phe Gln Leu  
115 120 125

Phe Val Pro Asp Asn Val Leu Lys Asn Met Val Val Gln Thr Asn Met  
130 135 140

Tyr Ala Lys Lys Phe Gln Glu Arg Phe Gly Ser Asp Gly Ala Trp Val  
145 150 155 160

Glu Val Thr Leu Thr Glu Met Lys Ala Phe Leu Gly Tyr Met Ile Ser  
165 170 175

Thr Ser Ile Ser His Cys Glu Ser Val Leu Ser Ile Trp Ser Gly Gly  
180 185 190

Phe Tyr Ser Asn Arg Ser Leu Ala Leu Val Met Ser Gln Ala Arg Phe

195	200	205
Glu Lys Ile Leu Lys Tyr Phe His Val Val Ala Phe Arg Ser Ser Gln 210 215 220		
Thr Thr His Gly Leu Tyr Lys Val Gln Pro Phe Leu Asp Ser Ser Leu Gln 225 230 235 240		
Asn Ser Phe Asp Ser Ala Phe Arg Pro Ser Gln Thr Gln Val Leu His 245 250 255		
Glu Pro Leu Ile Asp Glu Asp Pro Val Phe Ile Ala Thr Cys Thr Glu 260 265 270		
Arg Glu Leu Arg Lys Arg Lys Lys Arg Lys Phe Ser Leu Trp Val Arg 275 280 285		
Gln Cys Ser Ser Thr Gly Phe Ile Ile Gln Ile Tyr Val His Leu Lys 290 295 300		
Glu Gly Gly Gly Pro Asp Gly Leu Asp Ala Leu Lys Asn Lys Pro Gln 305 310 315 320		
Leu His Ser Met Val Ala Arg Ser Leu Cys Arg Asn Ala Ala Gly Lys 325 330 335		
Asn Tyr Ile Ile Phe Thr Gly Pro Ser Ile Thr Ser Leu Thr Leu Phe 340 345 350		
Glu Glu Phe Glu Lys Gln Gly Ile Tyr Cys Cys Gly Leu Leu Arg Ala 355 360 365		
Arg Lys Ser Asp Cys Thr Gly Leu Pro Leu Ser Met Leu Thr Asn Pro 370 375 380		
Ala Thr Pro Pro Ala Arg Gly Gln Tyr Gln Ile Lys Met Lys Gly Asn 385 390 395 400		
Met Ser Leu Ile Cys Trp Tyr Asn Lys Gly His Phe Arg Phe Leu Thr 405 410 415		
Asn Ala Tyr Ser Pro Val Gln Gln Gly Val Ile Ile Lys Arg Lys Ser 420 425 430		
Gly Glu Ile Pro Cys Pro Leu Ala Val Glu Ala Phe Ala Ala His Leu 435 440 445		

Ser Tyr Ile Cys Arg Tyr Asp Asp Lys Tyr Ser Lys Tyr Phe Ile Ser  
450 455 460

His Lys Pro Asn Lys Thr Trp Gln Gln Val Phe Trp Phe Ala Ile Ser  
465 470 475 480

Ile Ala Ile Asn Asn Ala Tyr Ile Leu Tyr Lys Met Ser Asp Ala Tyr  
485 490 495

His Val Lys Arg Tyr Ser Arg Ala Gln Phe Gly Glu Arg Leu Val Arg  
500 505 510

Glu Leu Leu Gly Leu Glu Asp Ala Ser Pro Thr His  
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<210> 8  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (162)..(635)  
<223> 1st open reading frame

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agggtaacac caaatcacta aacagcactg ttgttacaga a atg tcg aaa agc tgt 176  
Met Ser Lys Ser Cys  
1 5  
gga aat aat tta gcg gcc att tct gta gga att tcg ctt ctt tta ctc 224  
Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile Ser Leu Leu Leu Leu  
10 15 20  
tta gtg gtt tgt gga att ggg tgt gtt tgg cac tgg aaa cac cgt gtt 272  
Leu Val Val Cys Gly Ile Gly Cys Val Trp His Trp Lys His Arg Val  
25 30 35  
gcc aca cga ttt acc tta ccg agg ttt tta caa agg aga agc agc agg 320  
Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln Arg Arg Ser Ser Arg  
40 45 50  
aga aaa gtc tgt act aaa aca ttc ttg ggc ccc cgc atc att ggc tta 368  
Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro Arg Ile Ile Gly Leu  
55 60 65  
agg cat gaa atc tca gtt gaa acc caa gac cac aaa tct gct gtc agg 416  
Arg His Glu Ile Ser Val Glu Thr Gln Asp His Lys Ser Ala Val Arg  
70 75 80 85



gga aat aac aca cac gac aac tat gaa aat gtg gaa gca ggt cct ccc Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val Glu Ala Gly Pro Pro	464
90 95 100	
aaa gct aaa gga aaa acc gat aag gaa cta tat gaa aac aca ggg cag Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr Glu Asn Thr Gly Gln	512
105 110 115	
tct aat ttc gag gag cat atc tat gga aat gag aca tct tct gac tat Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu Thr Ser Ser Asp Tyr	560
120 125 130	
tat aac ttc cag aag cct cgt cct tct gaa gtt cct caa gat gaa gat Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val Pro Gln Asp Glu Asp	608
135 140 145	
ata tac att ctt cca gat tca tat tag cttttcaaaa tattgacttt Ile Tyr Ile Leu Pro Asp Ser Tyr	655
150 155	
tgttattgga tgataaatat tcaactgtaat ttttcaacag caaagacaag gaatcaaact	715
aaatgttgat caactgtaga ctggataaag aaaatgtggg acacatacac catagaatat	775
tatgcagccg taaaaaaga acaaaactaa catgggaaca gaaatcaaa taccacatat	835
tctcacttaa aagtgggagc taaataataa gaacacatgg agagaaggag aggaacaaca	895
gacactgggg cctacttgag ggaggacagt ggaaggaggg agaggttcag ggaaaaaaa	955
aatatcaggt actatgctta gtacacacat gatgaaataa tctgtacacc aaacccccaa	1015
gtcacaagtg ttctacata acaaacctga acatgtaccc ctgaacataa aattataatt	1075
aaaatattaa aaataattca ctgtgatttt tattgtactg atgccattct taatcaagtt	1135
ctgataagtg gatggctctc gcctatctcc acctttctga atcctatgtg tatcgctgtg	1195
gattaattct agatatcttc tccacctctc ttgcaccaga ctaaactctg attatgtgat	1255
attgattctt ccttctaatt attaccogtt atctctttcc tttattttcta coattatctt	1315
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cattttatta ctagcttca tatgaaatg tcttaaatc ccacctaaat gaaaagaac	1855

tgcccaaatg cctagaacat cacataaggc actaaatgcc tcattgttta ctgacgggaa 1915  
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 tcattccataa aaaaaaaaaa aaa 1998

<210> 9  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 9

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Ser Leu Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His  
 20 25 30

Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln  
 35 40 45

Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro  
 50 55 60

Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His  
 65 70 75 80

Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val  
 85 90 95

Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr  
 100 105 110

Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu  
 115 120 125

Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val  
 130 135 140

Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> (373)..(651)  
 <223> 2nd open reading frame

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agggtaacac caaatcacta aacagcactg tttgtacaga aatgtcgaaa agctgtggaa      180
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tacaaaggag aagcagcagg agaaaagtct gtactaaaac attcttgggc cccgcgatca      360
ttggcttaag gc atg aaa tct cag ttg aaa ccc aag acc aca aat ctg ctg      411
                Met Lys Ser Gln Leu Lys Pro Lys Thr Thr Asn Leu Leu
                1          5          10
tca ggg gaa ata aca cac acg aca act atg aaa atg tgg aag cag gtc      459
Ser Gly Glu Ile Thr His Thr Thr Met Lys Met Trp Lys Gln Val
                15          20          25
ctc cca aag cta aag gaa aaa ccg ata agg aac tat atg aaa aca cag      507
Leu Pro Lys Leu Lys Glu Lys Pro Ile Arg Asn Tyr Met Lys Thr Gln
                30          35          40          45
ggc agt cta att tog agg agc ata tct atg gaa atg aga cat ctt ctg      555
Gly Ser Leu Ile Ser Arg Ser Ile Ser Met Glu Met Arg His Leu Leu
                50          55          60
act att ata act tcc aga agc ctc gtc ctt ctg aag ttc ctc aag atg      603
Thr Ile Ile Thr Ser Arg Ser Leu Val Leu Leu Lys Phe Leu Lys Met
                65          70          75
aag ata tat aca ttc ttc cag att cat att agc ttt tca aaa tat tga      651
Lys Ile Tyr Thr Phe Phe Gln Ile His Ile Ser Phe Ser Lys Tyr
                80          85          90
cttttgttat tggatgataa atattcactg taatttttca acagcaaaga caaggaatca      711
aactaaatgt tgatcaactg tagactggat aaagaaaatg tggtagacat acaccataga      771
atattatgca gccgtaaaaa aagaacaaaa ctaacatggg aacagaaaaa caaataccac      831
atattctcac ttaaaagtgg gagctaaata ataagaacac atggagagaa ggagaggaac      891
aacagacact ggggcctact tgagggagga cagtgggaagg agggagaggt tcagggaaaa      951
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aaactgccca aatgcctaga acatcacata aggcactaaa tgccctcatgt tttactgacg 1911  
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ttattcatcc ataaaaaaaa aaaaaaa 1998

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<211> 92  
<212> PRT  
<213> Homo sapiens

<400> 11

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Ile Thr His Thr Thr Thr Met Lys Met Trp Lys Gln Val Leu Pro Lys  
20 25 30

Leu Lys Glu Lys Pro Ile Arg Asn Tyr Met Lys Thr Gln Gly Ser Leu  
35 40 45

Ile Ser Arg Ser Ile Ser Met Glu Met Arg His Leu Leu Thr Ile Ile  
50 55 60

Thr Ser Arg Ser Leu Val Leu Leu Lys Phe Leu Lys Met Lys Ile Tyr  
65 70 75 80

Thr Phe Phe Gln Ile His Ile Ser Phe Ser Lys Tyr  
85 90

<210> 12  
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1662)

<223>

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cag ctc ttg ctg gtc aac ctg cta acc ttt ggc ctg gag gtg tgt ttg 96  
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
20 25 30  
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Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val  
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Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
50 55 60  
ctg gtc tgt gtc ccg ctc cta ggc tca gcc agt gac cac tgg cgt gga 240  
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
65 70 75 80  
cgc tat ggc cgc cgc cgg ccc ttc atc tgg gca ctg tcc ttg ggc atc 288  
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
85 90 95  
ctg ctg agc ctc ttt ctc atc cca agg gcc ggc tgg cta gca ggg ctg 336  
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
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Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
115 120 125  
gtg ggg ctg ctg gac ttc tgt ggc cag gtg tgc ttc act cca ctg gag 432  
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
130 135 140  
gcc ctg ctc tct gac ctc ttc cgg gac ccg gac cac tgt cgc cag gcc 480  
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
145 150 155 160  
tac tct gtc tat gcc ttc atg atc agt ctt ggg ggc tgc ctg ggc tac 528  
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
165 170 175  
ctc ctg cct gcc att gac tgg gac acc agt gcc ctg gcc ccc tac ctg 576  
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
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ggc acc cag gag gag tgc ctc ttt ggc ctg ctc acc ctc atc ttc ctc 624  
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
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 Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Glu Val Gly Val  
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 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
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 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65 70 75 80  
 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85 90 95  
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
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Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
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Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
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Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
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Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
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Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
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Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
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Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
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Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
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Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
340 345 350



Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
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Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
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Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
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Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
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Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
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Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
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Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
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Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
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Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
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Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
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Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
545 550